

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/016,869BDATE: 03/26/2002
TIME: 21:16:41

INPUT SET: S36811.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Beach, David H.
6 Demetrick, Douglas J.
7 Serrano, Manuel
8 Hannon, Gregory J.
9
10 (ii) TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and
11 Uses Related Thereto
12
13 (iii) NUMBER OF SEQUENCES: 35
14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Ropes & Gray
17 (B) STREET: One International Place
18 (C) CITY: Boston
19 (D) STATE: MA
20 (E) COUNTRY: USA
21 (F) ZIP: 02110
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: WordPad
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: US 09/016,869
31 (B) FILING DATE: 30-JAN-1998
32
33
34 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: US 08/893,274
36 (B) FILING DATE: 15-JUL-1994
37
38 (vii) PRIOR APPLICATION DATA:
39 (A) APPLICATION NUMBER: US 08/306,511
40 (B) FILING DATE: 14-SEP-1994
41
42 (vii) PRIOR APPLICATION DATA:
43 (A) APPLICATION NUMBER: US 08/248,812
44 (B) FILING DATE: 25-MAY-1994
45
46 (vii) PRIOR APPLICATION DATA:

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47      (A) APPLICATION NUMBER: US 08/227,371
48      (B) FILING DATE: 14-APR-1994
49
50      (vii) PRIOR APPLICATION DATA:
51          (A) APPLICATION NUMBER: US 08/154,915
52          (B) FILING DATE: 18-NOV-1993
53
54      (vii) PRIOR APPLICATION DATA:
55          (A) APPLICATION NUMBER: US 07/991,997
56          (B) FILING DATE: 17-DEC-1992
57
58      (viii) ATTORNEY/AGENT INFORMATION:
59          (A) NAME: Vincent, Matthew P.
60          (B) REGISTRATION NUMBER: 36,709
61          (C) REFERENCE/DOCKET NUMBER: GPCI-P10-071
62
63      (ix) TELECOMMUNICATION INFORMATION:
64          (A) TELEPHONE: (617) 951-7739
65          (B) TELEFAX: (617) 951-7050
66
67
68      (2) INFORMATION FOR SEQ ID NO:1:
69          (i) SEQUENCE CHARACTERISTICS:
70              (A) LENGTH: 994 base pairs
71              (B) TYPE: nucleic acid
72              (C) STRANDEDNESS: both
73              (D) TOPOLOGY: linear
74
75          (ii) MOLECULE TYPE: cDNA
76          (ix) FEATURE:
77              (A) NAME/KEY: CDS
78              (B) LOCATION: 41..508
79
80          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
81
82      CCGAGAGGGG GAGAACAGAC AACGGGCGGC GGGGAGCAGC ATG GAT CCG GCG GCG      55
83                                     Met Asp Pro Ala Ala
84                                     1      5
85      GGG AGC AGC ATG GAG CCT TCG GCT GAC TGG CTG GCC ACG GCC GCG GCC      103
86      Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu Ala Thr Ala Ala Ala
87               10      15      20
88      CGG GGT CGG GTA GAG GAG GTG CGG GCG CTG CTG GAG GCG GTG GCG CTG      151
89      Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu Glu Ala Val Ala Leu
90               25      30      35
91      CCC AAC GCA CCG AAT AGT TAC GGT CGG AGG CCG ATC CAG GTC ATG ATG      199
92      Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro Ile Gln Val Met Met
93               40      45      50
94      ATG GGC AGC GCC CGA GTG GCG GAG CTG CTG CTG CTC CAC GGC GCG GAG      247
95      Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly Ala Glu
96               55      60      65
97      CCC AAC TGC GCC GAC CCC GCC ACT CTC ACC CGA CCC GTG CAC GAC GCT      295
98      Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala
99      70      75      80      85

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100  GCC CGG GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG      343
101  Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly
102                90                95                100
103  GCG CGG CTG GAC GTG CGC GAT GCC TGG GGC CGT CTG CCC GTG GAC CTG      391
104  Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu
105                105                110                115
106  GCT GAG GAG CTG GGC CAT CGC GAT GTC GCA CGG TAC CTG CGC GCG GCT      439
107  Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala
108                120                125                130
109  GCG GGG GGC ACC AGA GGC AGT AAC CAT GCC CGC ATA GAT GCC GCG GAA      487
110  Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg Ile Asp Ala Ala Glu
111                135                140                145
112  GGT CCC TCA GAC ATC CCC GAT TGAAAGAACC AGAGAGGCTC TGAGAAACCT      538
113  Gly Pro Ser Asp Ile Pro Asp
114  150                155
115  CGGGAAACTT AGATCATCAG TCACCGAAGG TCCTACAGGG CCACAACTGC CCCC GCCACA      598
116  ACCACCCCG CTTTCGTAGT TTTTATTTAG AAAATAGAGC TTTTAAAAAT GTCCTGCCTT      658
117  TTAACGTAGA TATAAGCCTT CCCCCACTAC CGTAAATGTC CATTATATATC ATTTTATATA      718
118  TATTCTTATA AAAATGTAAA AAAGAAAAAC ACCGCTTCTG CCTTTTCACT GTGTTGGAGT      778
119  TTTCTGGAGT GAGCACTCAC GCCCTAAGCG CACATTCATG TGGGCATTTC TTGCGAGCCT      838
120  CGCAGCCTCC GGAAGCTGTC GACTTCATGA CAAGCATTTC GTGAAGTAGG GAAGCTCAGG      898
121  GGGGTACTG GCTTCTCTTG AGTCACACTG CTAGCAAATG GCAGAACCAA AGCTCAAATA      958
122  AAAATAAAAT TATTTTCATT CATTCACTCA AAAAAA      994

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123

124 (2) INFORMATION FOR SEQ ID NO:2:

125

126 (i) SEQUENCE CHARACTERISTICS:

127 (A) LENGTH: 156 amino acids

128 (B) TYPE: amino acid

129 (D) TOPOLOGY: linear

130

131 (ii) MOLECULE TYPE: protein

132

133 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

134

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135  Met Asp Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
136    1          5          10          15
137  Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
138          20          25          30
139  Glu Ala Val Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
140          35          40          45
141  Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
142          50          55          60
143  Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg
144          65          70          75          80
145  Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val
146          85          90          95
147  Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg
148          100          105          110
149  Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg
150          115          120          125
151  Tyr Leu Arg Ala Ala Ala Gly Thr Arg Gly Ser Asn His Ala Arg
152          130          135          140

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153 Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
154 145 150 155

156 (2) INFORMATION FOR SEQ ID NO:3:

157 (i) SEQUENCE CHARACTERISTICS:

158 (A) LENGTH: 837 base pairs

159 (B) TYPE: nucleic acid

160 (C) STRANDEDNESS: single

161 (D) TOPOLOGY: linear

162 (ii) MOLECULE TYPE: cDNA

163 (ix) FEATURE:

164 (A) NAME/KEY: CDS

165 (B) LOCATION: 328..738

166 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

170
171 GAGGACTCCG CGACGGTCCG CACCCTGCGG CCAGAGCGGC TTTGAGCTCG GCTGCTTCCG      60
172 CGCTAGGCGC TTTTTCCTCAG AAGCAATCCA GGCGCGCCCG CTGGTTCTTG AGCGCCAGGA      120
173 AAAGCCCGGA GCTAACGACC GGCCGCTCGG CACTGCACGG GGCCCCAAGC CGCAGAAGAA      180
174 GGACGACGGG AGGGTAATGA AGCTGAGCCC AGGTCTCCTA GGAAGGAGAG AGTGCGCCCG      240
175 AGCAGCGTGG GAAAGAAGGG AAGAGTGTCT TTAAGTTTAC GGCCAACGGT GGATTATCCG      300
176 GGCCGCTGCG CGTCTGGGGG CTGCGGA ATG CGC GAG GAG AAC AAG GGC ATG      351
177                               Met Arg Glu Glu Asn Lys Gly Met
178                               1           5
179 CCC AGT GGG GGC GGC AGC GAT GAG GGT CTG GCC ACG CCG GCG CGG GGA      399
180 Pro Ser Gly Gly Gly Ser Asp Glu Gly Leu Ala Thr Pro Ala Arg Gly
181 10           15           20
182 CTA GTG GAG AAG GTG CGA CAC TCC TGG GAA GCC GGC GCG GAT CCC AAC      447
183 Leu Val Glu Lys Val Arg His Ser Trp Glu Ala Gly Ala Asp Pro Asn
184 25           30           35           40
185 GGA GTC AAC CGT TTC GGG AGG CGC GCG ATC CAG GTC ATG ATG ATG GGC      495
186 Gly Val Asn Arg Phe Gly Arg Arg Ala Ile Gln Val Met Met Met Gly
187 45           50           55
188 AGC GCC CGC GTG GCG GAG CTG CTG CTG CTC CAC GGC GCG GAG CCC AAC      543
189 Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly Ala Glu Pro Asn
190 60           65           70
191 TGC GCA GAC CCT GCC ACT CTC ACC CGA CCG GTG CAT GAT GCT GCC CGG      591
192 Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala Ala Arg
193 75           80           85
194 GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG GCG CGG      639
195 Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg
196 90           95           100
197 CTG GAC GTG CGC GAT GCC TGG GGT CGT CTG CCC GTG GAC TTG GCC GAG      687
198 Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu
199 105          110          115          120
200 GAG CGG GGC CAC CGC GAC GTT GCA GGG TAC CTG CGC ACA GCC ACG GGG      735
201 Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Thr Ala Thr Gly
202 125          130          135
203 GAC TGACGCCAGG TTCCCAGCC GCCACAACG ACTTTATTTT CTTACCCAAT      788
204 Asp
205

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206 TTCCACCCCC CACCCACCTA ATTCGATGAA GGCTGCCAAC GGGGAGCGG 837
207
208 (2) INFORMATION FOR SEQ ID NO:4:
209
210 (i) SEQUENCE CHARACTERISTICS:
211 (A) LENGTH: 137 amino acids
212 (B) TYPE: amino acid
213 (D) TOPOLOGY: linear
214
215 (ii) MOLECULE TYPE: protein
216
217 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
218
219 Met Arg Glu Glu Asn Lys Gly Met Pro Ser Gly Gly Gly Ser Asp Glu
220 1 5 10 15
221 Gly Leu Ala Thr Pro Ala Arg Gly Leu Val Glu Lys Val Arg His Ser
222 20 25 30
223 Trp Glu Ala Gly Ala Asp Pro Asn Gly Val Asn Arg Phe Gly Arg Arg
224 35 40 45
225 Ala Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu
226 50 55 60
227 Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr
228 65 70 75 80
229 Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val
230 85 90 95
231 Val Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly
232 100 105 110
233 Arg Leu Pro Val Asp Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala
234 115 120 125
235 Gly Tyr Leu Arg Thr Ala Thr Gly Asp
236 130 135
237
238 (2) INFORMATION FOR SEQ ID NO:5:
239
240 (i) SEQUENCE CHARACTERISTICS:
241 (A) LENGTH: 853 base pairs
242 (B) TYPE: nucleic acid
243 (C) STRANDEDNESS: both
244 (D) TOPOLOGY: linear
245
246 (ii) MOLECULE TYPE: cDNA
247
248 (ix) FEATURE:
249 (A) NAME/KEY: CDS
250 (B) LOCATION: 213..587
251
252 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
253
254 GGAGTACAGC AGCGGGAGCA TGGGTCGCAG GTTCTTGGTC ACTGTAAGGA TTCAGCGCGC 60
255
256 GGGCCGCCCA CTCCAAGAGA GGGTTTTCTT GGTGAAGTTC GTGCGATCCC GGAGACCCAG 120
257
258 GACAGCGAGC TGCCTCTGG CTTTCGTGAA CATGTTGTTG AGGCTAGAGA GGATCTTGAG 180

PAGE: 1

SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text